SEQUENCE LISTING

<110> Giger, Roman J.

<120> IDENTIFICATION OF NOVEL NOGO-RECEPTORS
      AND METHODS RELATED THERETO

<130> 21108.0028U2

<140> 10/551,833
<141> 2005-10-03

<150> PCT/US04/010328
<151> 2004-04-02

<150> 60/460,849
<151> 2003-04-04

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 1
Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1   5   10   15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
            20   25   30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
            35   40   45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
        50   55   60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65   70   75   80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
                85   90   95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
            100   105   110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
            115   120   125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
        130   135   140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145   150   155   160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
                165   170   175

```
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
            180                 185                 190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
            195                 200                 205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
            210                 215                 220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
225                 230                 235                 240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
                245                 250                 255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
            260                 265                 270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
        275                 280                 285
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
        290                 295                 300
Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Phe Gln
305                 310                 315                 320
Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys Cys
                325                 330                 335
Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro
            340                 345                 350
Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr
        355                 360                 365
Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe
    370                 375                 380
Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro
385                 390                 395                 400
Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg
                405                 410                 415
Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly
            420                 425                 430
Gln Ala Gly Ser Gly Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly
        435                 440                 445
Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu
    450                 455                 460
Val Leu Trp Thr Val Leu Gly Pro Cys
465                 470
```

```
<210> 2
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 2
Pro Val Thr Pro Ser Cys Pro Met Leu Cys Thr Cys Tyr Ser Ser Pro
 1               5                 10                  15
Pro Thr Val Ser Cys Gln Ala Asn Asn Phe Ser Ser Val Pro Leu Ser
            20                  25                  30
Leu Pro Pro Ser Thr Gln Arg Leu Phe Leu Gln Asn Asn Leu Ile Arg
        35                  40                  45
Ser Leu Arg Pro Gly Thr Phe Gly Pro Asn Leu Leu Thr Leu Trp Leu
    50                  55                  60
```

```
Phe Ser Asn Asn Leu Ser Thr Ile Tyr Pro Gly Thr Phe Arg His Leu
65                  70              75                      80
Gln Ala Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg His Leu Arg Ser
                85              90                  95
Leu Glu Pro Asp Thr Phe Gln Gly Leu Glu Arg Leu Gln Ser Leu His
            100             105             110
Leu Tyr Arg Cys Gln Leu Ser Ser Leu Pro Gly Asn Ile Phe Arg Gly
        115             120             125
Leu Val Ser Leu Gln Tyr Leu Tyr Leu Gln Glu Asn Ser Leu Leu His
    130             135             140
Leu Gln Asp Asp Leu Phe Ala Asp Leu Ala Asn Leu Ser His Leu Phe
145             150             155                     160
Leu His Gly Asn Arg Leu Arg Leu Leu Thr Glu His Val Phe Arg Gly
            165             170             175
Leu Gly Ser Leu Asp Arg Leu Leu Leu His Gly Asn Arg Leu Gln Gly
        180             185             190
Val His Arg Ala Ala Phe His Gly Leu Ser Arg Leu Thr Ile Leu Tyr
        195             200             205
Leu Phe Asn Asn Ser Leu Ala Ser Leu Pro Gly Glu Ala Leu Ala Asp
    210             215             220
Leu Pro Ala Leu Glu Phe Leu Arg Leu Asn Ala Asn Pro Trp Ala Cys
225             230             235                     240
Asp Cys Arg Ala Arg Pro Leu Trp Ala Trp Phe Gln Arg Ala Arg Val
            245             250             255
Ser Ser Ser Asp Val Thr Cys Ala Thr Pro Pro Glu Arg Gln Gly Arg
            260             265             270
Asp Leu Arg Thr Leu Arg Asp Thr Asp Phe Gln Ala Cys Pro
            275             280             285
```

<210> 3
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 3
```
Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
1               5               10                      15
Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
            20              25              30
Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
        35              40              45
Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
    50              55              60
Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
65              70              75                      80
Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
            85              90                  95
Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
        100             105             110
Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
        115             120             125
Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
    130             135                 140
```

```
Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
145                 150                 155                 160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
                165                 170                 175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
                180                 185                 190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
            195                 200                 205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
    210                 215                 220
Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
225                 230                 235                 240
Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
                245                 250                 255
Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
            260                 265                 270
Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
        275                 280                 285
Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
    290                 295                 300
Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
305                 310                 315                 320
Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
            325                 330                 335
Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
            340                 345                 350
Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
            355                 360                 365
Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr
    370                 375                 380
Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val
385                 390                 395                 400
Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala
                405                 410                 415
Pro His His Leu
            420
```

`<210> 4`
`<211> 175`
`<212> PRT`
`<213> Artificial Sequence`

`<220>`
`<223> Description of Artificial Sequence:/Note =`
`      Synthetic Construct`

`<400> 4`
```
Asn Gly Asn Ala Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu
1               5               10              15
Trp Leu Arg Arg Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr
            20              25              30
Pro Glu Leu Arg Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp
        35              40              45
Phe Arg Asn Cys Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His
    50              55              60
Thr Leu Ser Thr Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser
65              70              75              80
```

```
His Gly Ala Ser Arg Asp Lys Gly His Pro His Gly His Leu Pro Gly
                85              90                  95
Ser Arg Ser Gly Ser Lys Lys Pro Gly Lys Asn Cys Thr Ser His Arg
            100             105             110
Asn Arg Asn Gln Ile Ser Lys Gly Ser Ala Gly Lys Glu Leu Pro Glu
            115             120             125
Leu Gln Asp Tyr Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile
    130             135             140
Met Pro Thr Ala Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr
145             150             155             160
Pro Ile Arg Ala Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr
            165             170             175
```

<210> 5
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 5
```
Met Leu Arg Lys Gly Cys Cys Val Glu Leu Leu Leu Leu Leu Leu Ala
  1           5              10                  15
Gly Glu Leu Pro Leu Ser Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
            20              25                  30
Pro Ser Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Ile
            35              40                  45
Pro Glu Gly Ile Pro Glu Asp Ser Glu Arg Ile Phe Leu Gln Asn Asn
    50              55                  60
His Ile Thr Phe Leu Gln Gln Gly His Phe Ser Pro Ala Met Val Thr
65              70                  75                  80
Leu Trp Ile Tyr Ser Asn Asn Ile Thr Phe Ile Ala Pro Asn Thr Phe
                85              90                  95
Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
            100             105             110
Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
            115             120             125
Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ser Leu Pro Ala Gly Ile
    130             135             140
Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
145             150             155             160
Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
            165             170             175
His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Gln Gly Ile
            180             185             190
Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu Leu His Glu Asn Gln
            195             200             205
Leu Gln Trp Val His His Lys Ala Phe His Asp Leu His Arg Leu Thr
    210             215             220
Thr Leu Phe Leu Phe Asn Asn Ser Leu Thr Glu Leu Gln Gly Asp Cys
225             230             235             240
Leu Ala Pro Leu Val Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Ala
            245             250             255
Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Arg Arg
            260             265             270
```

```
Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr Pro Glu Leu Arg
        275             280             285
Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp Phe Arg Asn Cys
        290             295             300
Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Ser Thr
305             310             315             320
Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
            325             330             335
Arg Asp Lys Gly His Pro His Gly His Leu Pro Gly Ser Arg Ser Gly
            340             345             350
Ser Lys Lys Pro Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
        355             360             365
Ile Ser Lys Gly Ser Ala Gly Lys Glu Leu Pro Glu Leu Gln Asp Tyr
        370             375             380
Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
385             390             395             400
Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
            405             410             415
Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Val Ser
            420             425             430
Leu Leu Ala Trp Ile Leu Gly Leu Val Val Ser Leu Arg
            435             440             445
```

<210> 6
<211> 2215
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 6

```
tcgcggacac ggggcgcacg gaccgaccga ctaaccgact ccctgcgggt ctgcgctgcc    60
gaggggcgcg gacaccgtt gtccagggtc aacccagccc tttccatctc gtcgtgcccc   120
gccccgtccc gtcggggccg atggctcctt cagaggcacg gagtccgggg ggcgcagggt   180
agagctccgc agccccgcta cgtagcccgg gactcccggg tccttacgga gccccgcgga   240
gtccccgccg tctgtccggc gggataaggg agcgagtggg agcgccctcc ccccccgcc    300
gccccctccc ccgatcgtcg agacaagatg ctgcccgggc tccggcgcct gctgcaaggt   360
cctgcctcag cctgcctcct gctgacactc ctggccctcc tcctgtgac ccccagctgc    420
cctatgctct gcacctgcta ctcctctccg cccacagtga gctgccaggc caacaacttc   480
tcctcggtgc cgctgtcctt gccacccagt acacagcgac tcttcttgca gaacaacctc   540
attcgctcac tgcggccagg aactttggg cccaacctgc tcaccctgtg gctcttctcc   600
aacaacctct ccaccatcta ccctggcacc ttccgccatc tgcaggccct agaggaactg   660
gacctcggtg acaatcggca cctgcgctcc ctggagcctg acaccttcca gggcctggag   720
aggctgcagt cactacatct gtaccggtgc cagctcagca gtctgcctgg caacatcttc   780
cgaggcctgg tcagcctaca gtacctctac ctccaggaga acagcctgct ccacctacag   840
gatgacttgt cgccgacct ggccaacctg agccaccttt cctccacgg aaccgcctg    900
cggctgctca cggagcacgt gttccgcggc ttgggcagcc tggaccggct gctgctgcac   960
gggaaccggc tgcagggcgt acaccgcgca gccttccacg tctcagccg cctcaccatc  1020
ctttacctgt tcaacaacag cctggcctcg ctgccgggag aggcgctggc tgacctgcca  1080
gcgctcgagt tcctgcggct caacgccaac ccctgggcgt gcgactgccg cgctcggccg  1140
ctctgggctt ggttccagcg cgcgcgggtg tccagctccg acgtgacctg cgccaccccg  1200
cccgagcgcc agggccggga cctgcgcacg ctgcgcgaca ccgatttcca agcgtgcccg  1260
ccgcccacac ccacgcggcc gggcagccgc gcccgcggca acagctcttc caaccacctg  1320
tacggcgtgg ccgaggcggg cgctcccccc gcagacccat ccacgctcta ccgagacctg  1380
cccgccgagg actcgcgggg gcgtcaggc ggggacgcgc ccactgagga cgactactgg  1440
```

```
ggggggctacg gcggcgagga ccagcgaggc gagcagacgt gtcccggggc cgcgtgccag    1500
gcgcccgcgg actcgcgtgg ccccgtgctc tcggccgggc tgcgcacccc tctgctctgc    1560
ctcttgctcc tggctcccca tcacctctga ctgcggtgct ccgatggaag agaccacgtt    1620
cttcgccccg ctccccttct ctgccccacg gagctgaggc tccgaacttg ccccttgttt    1680
gcgacccggc ctggcacctt ccctaggcct cctcgctctt tttcttcccc tgaccaggct    1740
gcctcatttg ccttccgggc tgttgtgact tatgtatggc agcccctaag acggtgtata    1800
aggtggctcg gccccattcg ccctgattct agacattaac tcttctgccc ccatcccaag    1860
gctggggcgt gacaccccag gcagccgttg ctcctctctc cggggcccca cagtggactc    1920
ggaggggctt tttgtccgca gagcaccttc caccagcaga gcctttgaaa gctcccctg     1980
ggagcctccc ctcctccccc tttggaggga tgtctcagcg aggcccaggc tgcccctgga    2040
ccctgcttgt cctgatccct tcagcctcct gacaccggag aatactttc tcctaagtct     2100
acccaggaca ctttttaggt gcctggagag atttcctctc accatggccc ctgtgtggtg    2160
aagataaaag aaattgtttg ggggaaaaaa tttattaaaa aattctatta ttttt         2215
```

<210> 7
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 7
```
atgaagaggg cgtcctccgg aggaagccgg ctgctggcat gggtgttatg gctacaggcc      60
tggagggtag caacgccctg ccctggtgcc tgtgtgtgct acaatgagcc caaggtcaca     120
acaagctgcc cccagcaggg cctgcaggct gtacccactg gcatcccagc ctccagccag     180
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag ccgccagctt ccagtcatgc     240
cggaatctca ccatcctgtg gctgcactca aatgcgctgg ccgggattga tgccgcggcc     300
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc     360
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc     420
ggcctgcagg agctgggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac    480
ctacaagaca acaacctgca ggcacttccc gacaacacct tccgagacct gggcaacctc     540
acgcatctct ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc     600
ttgcacagtc ttgaccgtct cctcttgcac cagaaccatg tggctcgtgt gcacccacat     660
gccttccggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg     720
ctccccgcag aggtcctagt gcccctgagg tctctgcagt acctgcgact caatgacaac     780
ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt     840
tcctcatccg aggtgccctg caacctaccc caacgcctgg caggccgtga tctgaagcgc     900
ctggctgcca gtgacttaga gggttgtgct gtggcttcgg ggcccttccg tcccttccag     960
accaatcagc tcactgatga ggagctgctg ggcctcccca agtgctgcca gccggatgct    1020
gcagacaagg cctcagtact ggaacccggg aggccggcgt ctgctggaaa tgcactcaag    1080
ggacgtgtgc ctcccggtga cactccacca ggcaatggct caggcccacg gcacatcaat    1140
gactctccat ttgggacttt gccgggctct gcagagcccc cactgactgc cctgcggcct    1200
ggggggttccg agcccccggg actgcccacc acgggtcccc gcaggaggcc aggttgttcc    1260
agaaagaacc gcacccgtag ccactgccgt ctgggccagg caggaagtgg gagcagtgga    1320
actggggatg cagaaggttc ggggggccctg cctgccctgg cctgcagcct tgctcctctg    1380
ggccttgcac tggtactttg gacagtgctt gggccctgct ga                       1422
```

<210> 8
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<220>
<221> misc_feature
<222> (0)...(0)
<223> n = a, t, c, or g

<400> 8
```
tgcggccgcc ggcgctttcc cggagctggg ctgtgcgtgc gagcgccctt ttgcagcagc      60
cgctgcccga gggggcgggg aagaggggac atcggctagc cggccagggg gcggcgtccc     120
ccctcaaaac cgcctgcaaa gtgtttgggg cggcagaatc aggccgccgg ctcggtggag     180
caagccactc gccccggggc tgagagagcg cacggcgttg gttggcagcg ccgcggttgc     240
tagcaggcgc cggtgccctg ggcgccgngc ttgggctcac catgcccctg cgggaccggg     300
ccgccgggca caagcggatt cccggcttgc ccccgcctcg acgcgctcgg attagctgta     360
gctggcgccc agggatttga atctggaccc caggagggag cgcgcctagg ccgacctcgg     420
aacggcggcc ccgcggccaa catgcttcgc aaagggtgct gtgtggaatt gctgctgttg     480
ctgctggctg gagagctacc tctgagtggt ggttgtcctc gagactgtgt gtgctacccc     540
tcgcccatga ctgtcagttg ccaggcacac aactttgccg ccatccccga gggcatccca     600
gaggacagcg agcgcatctt cctgcagaac aatcacatca ccttcctcca gcagggccac     660
ttcagccccg ccatggtcac cctctggatc tactccaaca acatcacttt cattgctccc     720
aacacctttg agggctttgt gcatctggag gagctagacc ttggagacaa ccggcagctt     780
cgaacgctgg cacccgagac cttccaaggc ctggtgaagc ttcacgccct ctacctctac     840
aagtgcggac tgagctccct gcctgcgggc atctttggtg gcctgcacag cctgcagtac     900
ctctacttgc aggacaacca tattgagtac ctccaagatg acatctttgt ggacctggtc     960
aacctcagtc acttgtttct ccatggcaac aagctatgga gcctgggcca gggcatcttc    1020
cggggcctgg tgaacctgga ccggttgctg ctgcatgaga accagctaca gtgggtccac    1080
cacaaggctt tccatgacct ccacaggcta accaccctct ttctcttcaa caatagcctc    1140
accgagctgc agggtgactg cctggccccc ctggtggccc tggagtttct tcgcctcaat    1200
gggaatgctt gggactgtgg ctgccgggca cggtccctgt gggaatggct gcgaaggttc    1260
cgtggctcca gctctgttgt cccctgcgcg actccagagc tgcggcaagg acaggacctg    1320
aagtcgctga gggttgagga cttccggaac tgcactggac cagcgtctcc tcaccagatc    1380
aagtctcaca cgcttagcac ctctgacagg gctgcccgca aggagcacca tccctcccac    1440
ggtgcctcca gggacaaagg ccacccacat ggccatctgc ctggctccag gtcaggttcc    1500
aagaagccag gcaagaactg caccagccac aggaaccgaa accagatctc taaggggagc    1560
gctgggaaag agcttcctga actgcaggac tatgcccccg actatcagca caagttcagc    1620
tttgacatca tgcccactgc acgacccaag aggaagggca agtgtgcccg caggacccccc    1680
atccgtgccc ccagtggggt gcagcaggcc tcctcaggca cggccctcgg ggtctcactc    1740
ctggcctgga tactggggct ggtggtatct ctccgctgag gacccagggc accgtcaccc    1800
agcactgcca cctgtccagc aaggaaacag aatctttct tctttctttt tcttttcctc    1860
taagtggaag atctgctggg tttcaggaaa aggctgctaa aaccttcagt ccagtgtgga    1920
cctttttggt ggattaaagc ccaacggtac agctgtagac aggaaggga gcacatctta    1980
cctggctgtc ctgaccgagc acctccggac agtattccac tcagccagtg gtcaaagggc    2040
acaccaagtg agtcgttagt ggtgtcagga catgtgcccc ttgaagaaat gggcttgcgg    2100
aatcctggtc acttggaaag aagggctgaa ggaccctgct ggtttcggaa ggagcaggac    2160
tcagaacaag gctcacccag agtcagctgg ggcaaacagc aatctcagag cactcttggt    2220
cttgcctgag atcacttagt taactggccc tgtccaatcc tatgcctccc tcagtcccta    2280
cccatgaggg taatgcctct cattcctgaa gtctcaggca gtcctggcag acttgctggg    2340
gttcaagaac caatcaccaa aggagagatc gccagaggat gacatataga actttactcg    2400
taatgagagt cacacagaag gtgcagtttt acctatgt ccacttatat atatattctc      2460
actctgacca cacatccaca taatatatat atatatatta taaatatata aatgcacagg    2520
tcccccaacc cactccttac caaactgtat gtcttatcat gtttataaac tatacgggaa    2580
cctaaaaaaa aaaaagtgaa a                                              2601
```

<210> 9
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 9
Met Leu Arg Lys Gly Cys Cys Val Glu Leu Leu Leu Leu Leu Ala
1   5   10   15
Gly Glu Leu Pro Leu Ser Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
            20   25   30
Pro Ser Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Val
            35   40   45
Pro Glu Gly Ile Pro Glu Asp Ser Glu Arg Ile Phe Leu Gln Asn Asn
      50   55   60
His Ile Thr Phe Leu Gln Gln Gly His Phe Ser Pro Ala Met Val Thr
65   70   75   80
Leu Trp Ile Tyr Ser Asn Asn Ile Thr Phe Ile Ala Pro Asn Thr Phe
                85   90   95
Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
            100   105   110
Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
            115   120   125
Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ser Leu Pro Ala Gly Ile
      130   135   140
Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
145   150   155   160
Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
            165   170   175
His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Gln Gly Ile
            180   185   190
Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu Leu His Glu Asn Gln
      195   200   205
Leu Gln Trp Val His His Lys Ala Phe His Asp Leu His Arg Leu Thr
      210   215   220
Thr Leu Phe Leu Phe Asn Asn Ser Leu Thr Glu Leu Gln Gly Asp Cys
225   230   235   240
Leu Ala Pro Leu Val Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Ala
            245   250   255
Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Arg Arg
            260   265   270
Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr Pro Glu Leu Arg
      275   280   285
Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp Phe Arg Asn Cys
      290   295   300
Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Ser Thr
305   310   315   320
Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
            325   330   335
Arg Asp Lys Gly His Pro His Gly His Leu Pro Gly Ser Arg Ser Gly
            340   345   350
Ser Lys Lys Pro Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
      355   360   365
Ile Ser Lys Gly Ser Ala Gly Lys Glu Leu Pro Glu Leu Gln Asp Tyr
      370   375   380
Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
385   390   395   400
Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
            405   410   415

```
Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Val Ser
            420                 425             430
Leu Leu Ala Trp Ile Leu Gly Leu Val Val Ser Leu Arg
            435                 440             445


<210> 10
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 10
Met Ala Ala Trp Pro Ser Arg Val Gly Ala Trp Arg Pro Gly Ala Gly
  1               5                 10                15
Pro Pro Thr Ser Ala Arg Leu Pro Gly Arg Leu Gly Gln Leu Gly Pro
            20                  25                30
Trp Lys Lys Val Gly Cys Cys Val Glu Leu Leu Leu Leu Leu Val Ala
            35                  40                45
Ala Glu Leu Pro Leu Gly Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
      50                  55                60
Pro Ala Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Ile
65                  70                  75                  80
Pro Glu Gly Ile Pro Val Asp Ser Glu Arg Val Phe Leu Gln Asn Asn
                85                  90                  95
Arg Ile Gly Leu Leu Gln Pro Gly His Phe Ser Pro Ala Met Val Thr
            100                 105                 110
Leu Trp Ile Tyr Ser Asn Asn Ile Thr Tyr Ile His Pro Ser Thr Phe
            115                 120                 125
Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
      130                 135                 140
Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
145                 150                 155                 160
Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ala Leu Pro Ala Gly Val
                165                 170                 175
Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
            180                 185                 190
Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
            195                 200                 205
His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Pro Gly Thr
      210                 215                 220
Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu Leu His Glu Asn Gln
225                 230                 235                 240
Leu Gln Trp Val His His Lys Ala Phe His Asp Leu Arg Arg Leu Thr
                245                 250                 255
Thr Leu Phe Leu Phe Asn Asn Ser Leu Ser Glu Leu Gln Gly Glu Cys
            260                 265                 270
Leu Ala Pro Leu Gly Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Pro
            275                 280                 285
Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Gln Arg
            290                 295                 300
Phe Arg Gly Ser Ser Ser Ala Val Pro Cys Val Ser Pro Gly Leu Arg
305                 310                 315                 320
His Gly Gln Asp Leu Lys Leu Leu Arg Ala Glu Asp Phe Arg Asn Cys
                325                 330                 335
```

```
Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Thr Thr
            340             345             350
Thr Asp Arg Ala Ala Arg Lys Glu His His Ser Pro His Gly Pro Thr
            355             360             365
Arg Ser Lys Gly His Pro His Gly Pro Arg Pro Gly His Arg Lys Pro
    370             375             380
Gly Lys Asn Cys Thr Asn Pro Arg Asn Arg Asn Gln Ile Ser Lys Ala
385             390             395             400
Gly Ala Gly Lys Gln Ala Pro Glu Leu Pro Asp Tyr Ala Pro Asp Tyr
            405             410             415
Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala Arg Pro Lys Arg
            420             425             430
Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala Pro Ser Gly Val
            435             440             445
Gln Gln Ala Ser Ser Ala Ser Ser Leu Gly Ala Ser Leu Leu Ala Trp
    450             455             460
Thr Leu Gly Leu Ala Val Thr Leu Arg
465             470
```

```
<210> 11
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 11
Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
  1             5              10              15
Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
            20              25              30
Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
            35              40              45
Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
    50              55              60
Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
65              70              75              80
Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
            85              90              95
Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
            100             105             110
Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
            115             120             125
Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
            130             135             140
Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
145             150             155             160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
            165             170             175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
            180             185             190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
            195             200             205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
    210             215             220
```

```
Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
225             230             235                 240
Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
                245             250                 255
Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
                260             265             270
Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
            275             280             285
Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
            290             295             300
Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Ser Pro Phe Arg Pro Phe
305             310             315                 320
Gln Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys
                325             330             335
Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg
            340             345             350
Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp
            355             360             365
Thr Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro
370             375             380
Phe Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg
385             390             395                 400
Pro Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg
            405             410             415
Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu
            420             425             430
Gly Gln Ala Gly Ser Gly Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser
            435             440             445
Gly Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala
450             455                 460
Leu Val Leu Trp Thr Val Leu Gly Pro Cys
465             470
```

<210> 12
<211> 1425
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 12

```
atgctgcccg ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca    60
ctcctggccc tccctcctgt gacccccagc tgccctatgc tctgcacctg ctactcctct   120
ccgcccacag tgagctgcca ggccaacaac ttctcctcgg tgccgctgtc cttgccaccc   180
agtacacagc gactcttctt gcagaacaac ctcattcgct cactgcggcc aggaactttt   240
gggcccaacc tgctcaccct gtggctcttc tccaacaacc tctccaccat ctaccctggc   300
accttccgcc atctgcaggc cctagaggaa ctggacctcg gtgacaatcg gcacctgcgc   360
tccctggagc ctgacacctt ccagggcctg gagaggctgc agtcactaca tctgtaccgg   420
tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagcct acagtacctc   480
tacctccagg agaacagcct gctccaccta caggatgact tgttcgccga cctggccaac   540
ctgagccacc tttcctccca cgggaaccgc ctgcggctgc tcacggagca cgtgttccgc   600
ggcttgggca gcctggaccg gctgctgctg cacgggaacc ggctgcaggg cgtacaccgc   660
gcagccttcc acggtctcag ccgcctcacc atcctttacc tgttcaacaa cagcctggcc   720
tcgctgccgg gagaggcgct ggctgacctg ccagcgctcg agttcctgcg gctcaacgcc   780
aaccccctggg cgtgcgactg ccgcgctcgg ccgctctggg cttggttcca gcgcgcgcgg   840
```

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```
gtgtccagct ccgacgtgac ctgcgccacc ccgcccgagc gccagggccg ggacctgcgc      900
acgctgcgcg acaccgattt ccaagcgtgc ccgccgccca ctagtccctt ccgtcccttc      960
cagaccaatc agctcactga tgaggagctg ctgggcctcc ccaagtgctg ccagccggat     1020
gctgcagaca aggcctcagt actggaaccc gggaggccgg cgtctgctgg aaatgcactc     1080
aagggacgtg tgcctcccgg tgacactcca ccaggcaatg gctcaggccc acggcacatc     1140
aatgactctc catttgggac tttgccgggc tctgcagagc ccccactgac tgccctgcgg     1200
cctgggggtt ccgagccccc gggactgccc accacgggtc cccgcaggag gccaggttgt     1260
tccagaaaga accgcacccg tagccactgc cgtctgggcc aggcaggaag tgggagcagt     1320
ggaactgggg atgcagaagg ttcggggggcc ctgcctgccc tggcctgcag ccttgctcct     1380
ctgggccttg cactggtact ttggaccgtg ctcgggccct gctga                     1425
```

<210> 13
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 13
```
Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1               5                  10                  15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
            20                  25                  30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
        35                  40                  45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
    50                  55                  60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65                  70                  75                  80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
                85                  90                  95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
            100                 105                 110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
        115                 120                 125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
    130                 135                 140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145                 150                 155                 160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
                165                 170                 175
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
            180                 185                 190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
        195                 200                 205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
    210                 215                 220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
225                 230                 235                 240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
                245                 250                 255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
                260                 265                 270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
            275                 280                 285
```

```
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
    290                 295             300
Asp Leu Glu Gly Cys Ala Val Ala Thr Ser Pro Thr Arg Pro Gly Ser
305             310                 315                 320
Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
                325             330             335
Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
                340             345             350
Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
            355             360             365
Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr
    370                 375             380
Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val
385             390                 395                 400
Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala
                405             410             415
Pro His His Leu
            420
```

```
<210> 14
<211> 1263
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 14
atgaagaggg cgtcctccgg aggaagccgg ctgctggcat gggtgttatg gctacaggcc        60
tggagggtag caacgccctg ccctggtgcc tgtgtgtgct acaatgagcc caaggtcaca       120
acaagctgcc cccagcaggg cctgcaggct gtacccactg gcatcccagc ctccagccag       180
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag ccgccagctt ccagtcatgc       240
cggaatctca ccatcctgtg ctgcactca aatgcgctgg ccgggattga tgccgcggcc        300
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc       360
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc       420
ggcctgcagg agctggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac       480
ctacaagaca caacctgca ggcacttccc gacaacacct tccgagacct gggcaacctc        540
acgcatctct ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc       600
ttgcacagtc ttgaccgtct cctcttgcac cagaaccatg tggctcgtgt gcacccacat       660
gccttccggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg       720
ctccccgcag aggtcctagt gcccctgagg tctctgcagt acctgcgact caatgacaac       780
ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt       840
tcctcatccg aggtgccctg caacctaccc caacgcctgg caggccgtga tctgaagcgc       900
ctggctgcca gtgacttaga gggttgtgct gtggctacta gtcccacgcg gccgggcagc       960
cgcgcccgcg gcaacagctc ttccaaccac ctgtacggcg tggccgaggc gggcgctccc      1020
cccgcagacc catccacgct ctaccgagac ctgcccgccg aggactcgcg ggggcgtcag      1080
ggcggggacg cgcccactga ggacgactac tggggggggct acggcggcga ggaccagcga      1140
ggcgagcaga cgtgtcccgg ggccgcgtgc caggcgcccg cggactcgcg tggccccgtg      1200
ctctcggccg ggctgcgcac ccctctgctc tgcctcttgc tcctggctcc ccatcacctc      1260
tga                                                                    1263
```

```
<210> 15
<211> 415
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct

<400> 15
Met Leu Arg Lys Gly Cys Cys Val Glu Leu Leu Leu Leu Leu Ala
1   5   10   15
Gly Glu Leu Pro Leu Ser Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
            20   25   30
Pro Ser Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Ile
            35   40   45
Pro Glu Gly Ile Pro Glu Asp Ser Glu Arg Ile Phe Leu Gln Asn Asn
    50   55   60
His Ile Thr Phe Leu Gln Gln Gly His Phe Ser Pro Ala Met Val Thr
65   70   75   80
Leu Trp Ile Tyr Ser Asn Asn Ile Thr Phe Ile Ala Pro Asn Thr Phe
                85   90   95
Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
            100   105   110
Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
        115   120   125
Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ser Leu Pro Ala Gly Ile
    130   135   140
Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
145   150   155   160
Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
            165   170   175
His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Gln Gly Ile
        180   185   190
Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu Leu His Glu Asn Gln
        195   200   205
Leu Gln Trp Val His His Lys Ala Phe His Asp Leu His Arg Leu Thr
    210   215   220
Thr Leu Phe Leu Phe Asn Asn Ser Leu Thr Glu Leu Gln Gly Asp Cys
225   230   235   240
Leu Ala Pro Leu Val Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Ala
            245   250   255
Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Arg Arg
        260   265   270
Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr Pro Glu Leu Arg
        275   280   285
Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp Phe Arg Asn Cys
    290   295   300
Thr Gly Pro Thr Ser Pro Thr Arg Pro Gly Ser Arg Ala Arg Gly Asn
305   310   315   320
Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu Ala Gly Ala Pro Pro
                325   330   335
Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro Ala Glu Asp Ser Arg
            340   345   350
Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp Asp Tyr Trp Gly Gly
        355   360   365
Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr Cys Pro Gly Ala Ala
    370   375   380
Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val Leu Ser Ala Gly Leu
385   390   395   400
Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala Pro His His Leu
                405   410   415

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<210> 16
<211> 1245
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 16
```
atgcttcgca aagggtgctg tgtggaattg ctgctgttgc tgctggctgg agagctacct      60
ctgagtggtg gttgtcctcg ctgtgtgtgc tacccctcgc ccatgactgt cagttgccag     120
gcacacaact ttgccgccat ccccgagggc atcccagagg acagcgagcg catcttcctg     180
cagaacaatc acatcacctt cctccagcag ggccacttca gccccgccat ggtcaccctc     240
tggatctact ccaacaacat cactttcatt gctcccaaca cctttgaggg ctttgtgcat     300
ctggaggagc tagaccttgg agacaaccgg cagcttcgaa cgctggcacc cgagaccttc     360
caaggcctgg tgaagcttca cgccctctac ctctacaagt gcggactgag ctccctgcct     420
gcgggcatct ttggtggcct gcacagcctg cagtacctct acttgcagga caaccatatt     480
gagtacctcc aagatgacat ctttgtggac ctggtcaacc tcagtcactt gtttctccat     540
ggcaacaagc tatggagcct gggccagggc atcttccggg gcctggtgaa cctggaccgg     600
ttgctgctgc atgagaacca gctacagtgg gtccaccaca aggctttcca tgacctccac     660
aggctaacca ccctctttct cttcaacaat agcctcaccg agctgcaggg tgactgcctg     720
gcccccctgg tggccctgga gtttcttcgc ctcaatggga atgcttggga ctgtggctgc     780
cgggcacggt ccctgtggga atggctgcga aggttccgtg ctccagctc tgttgtcccc      840
tgcgcgactc cagagctgcg gcaaggacag gacctgaagt cgctgagggt tgaggacttc     900
cggaactgca ctggaccaac tagtcccacg cggccgggca gccgcgcccg cggcaacagc     960
tcttccaacc acctgtacgg cgtggccgag gcgggcgctc cccccgcaga cccatccacg    1020
ctctaccgag acctgcccgc cgaggactcg cggggggcgtc agggcgggga cgcgcccact    1080
gaggacgact actggggggg ctacggcggc gaggaccagc gaggcgagca gacgtgtccc    1140
ggggccgcgt gccaggcgcc cgcggactcg cgtggccccg tgctctcggc cgggctgcgc    1200
accccctctgc tctgcctctt gctcctggct ccccatcacc tctga                   1245
```

<210> 17
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 17
```
Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
 1               5                  10                  15
Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
            20                  25                  30
Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
         35                  40                  45
Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
     50                  55                  60
Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
65                  70                  75                  80
Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
                85                  90                  95
Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
               100                 105                 110
```

```
Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
        115                 120                 125
Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
    130                 135                 140
Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
145                 150                 155                 160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
                165                 170                 175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
            180                 185                 190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
        195                 200                 205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
    210                 215                 220
Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
225                 230                 235                 240
Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
                245                 250                 255
Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
            260                 265                 270
Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
    275                 280                 285
Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
    290                 295                 300
Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
305                 310                 315                 320
Arg Ala Arg Gly Asn Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
            325                 330                 335
Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
        340                 345                 350
Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
    355                 360                 365
Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
    370                 375                 380
Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
385                 390                 395                 400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
            405                 410                 415
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
            420                 425                 430
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
        435                 440                 445
Leu Gly Pro Cys
        450
```

<210> 18
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 18
atgctgcccg ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca   60
ctcctggccc tccctcctgt dacccccagc tgccctatgc tctgcacctg ctactcctct   120

```
ccgcccacag tgagctgcca ggccaacaac ttctcctcgg tgccgctgtc cttgccaccc      180
agtacacagc gactcttctt gcagaacaac ctcattcgct cactgcggcc aggaactttt      240
gggcccaacc tgctcaccct gtggctcttc tccaacaacc tctccaccat ctaccctggc      300
accttccgcc atctgcaggc cctagaggaa ctggacctcg gtgacaatcg gcacctgcgc      360
tccctggagc ctgacacctt ccagggcctg gagaggctgc agtcactaca tctgtaccgg      420
tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagcct acagtacctc      480
tacctccagg agaacagcct gctccaccta caggatgact tgttcgccga cctggccaac      540
ctgagccacc ttttcctcca cgggaaccgc ctgcggctgc tcacggagca cgtgttccgc      600
ggcttgggca gcctggaccg gctgctgctg cacgggaacc ggctgcaggg cgtacaccgc      660
gcagccttcc acggtctcag ccgcctcacc atcctttacc tgttcaacaa cagcctggcc      720
tcgctgccgg gagaggcgct ggctgacctg ccagcgctcg agttcctgcg gctcaacgcc      780
aacccctggg cgtgcgactg ccgcgctcgg ccgctctggg cttggttcca gcgcgcgcgg      840
gtgtccagct ccgacgtgac ctgcgccacc ccgcccgagc gccagggccg ggacctgcgc      900
acgctgcgcg acaccgattt ccaagcgtgc ccgccgccca cacccacgcg gccgggcagc      960
cgcgccccgcg gcaacactag tcccgggagg ccggcgtctg ctggaaatgc actcaaggga     1020
cgtgtgcctc ccggtgacac tccaccaggc aatggctcag gcccacggca catcaatgac     1080
tctccatttg ggactttgcc gggctctgca gagcccccac tgactgccct gcggcctggg     1140
ggttccgagc ccccgggact gcccaccacg ggtccccgca ggaggccagg ttgttccaga     1200
aagaaccgca cccgtagcca ctgccgtctg ggccaggcag gaagtgggag cagtggaact     1260
ggggatgcag aaggttcggg ggccctgcct gccctggcct gcagccttgc tcctctgggc     1320
cttgcactgg tactttggac cgtgctcggg ccctgctga                            1359
```

<210> 19
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 19

```
Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1               5                  10                  15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
            20                  25                  30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
        35                  40                  45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
    50                  55                  60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65                  70                  75                  80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
                85                  90                  95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
            100                 105                 110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
        115                 120                 125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
    130                 135                 140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145                 150                 155                 160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
                165                 170                 175
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
            180                 185                 190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
```

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```
            195                 200                 205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
    210                 215                 220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
225                 230                 235                 240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
                245                 250                 255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
                260                 265                 270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
            275                 280                 285
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
    290                 295                 300
Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Phe Gln
305                 310                 315                 320
Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys Cys
                325                 330                 335
Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Thr Ser Ser Asn His Leu
                340                 345                 350
Tyr Gly Val Ala Glu Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu
            355                 360                 365
Tyr Arg Asp Leu Pro Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp
    370                 375                 380
Ala Pro Thr Glu Asp Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln
385                 390                 395                 400
Arg Gly Glu Gln Thr Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp
                405                 410                 415
Ser Arg Gly Pro Val Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys
            420                 425                 430
Leu Leu Leu Leu Ala Pro His His Leu
            435                 440
```

```
<210> 20
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 20
atgaagaggg cgtcctccgg aggaagccgg ctgctggcat gggtgttatg gctacaggcc    60
tggagggtag caacgccctg ccctggtgcc tgtgtgtgct acaatgagcc caaggtcaca   120
acaagctgcc cccagcaggg cctgcaggct gtacccactg gcatcccagc ctccagccag   180
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag ccgccagctt ccagtcatgc   240
cggaatctca ccatcctgtg ctgcactca aatgcgctgg ccgggattga tgccgcggcc   300
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc   360
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc   420
ggcctgcagg agctggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac   480
ctacaagaca caacctgca ggcacttccc gacaacacct tccgagacct gggcaacctc   540
acgcatctct ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc   600
ttgcacagtc ttgaccgtct cctcttgcac cagaaccatg tggctcgtgt gcacccacat   660
gccttccggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg   720
ctccccgcag aggtcctagt gcccctgagg tctctgcagt acctgcgact caatgacaac   780
ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt   840
tcctcatccg aggtgccctg caacctaccc caacgcctgg caggccgtga tctgaagcgc   900
```

```
ctggctgcca gtgacttaga gggttgtgct gtggcttcgg ggcccttccg tcccttccag    960
accaatcagc tcactgatga ggagctgctg ggcctcccca agtgctgcca gccggatgct   1020
gcagacaagg cctcagtaac tagttccaac cacctgtacg gcgtggccga ggcgggcgct   1080
ccccccgcag acccatccac gctctaccga gacctgcccg ccgaggactc gcgggggcgt   1140
cagggcgggg acgcgcccac tgaggacgac tactggggg gctacggcgg cgaggaccag   1200
cgaggcgagc agacgtgtcc cggggccgcg tgccaggcgc ccgcggactc gcgtggcccc   1260
gtgctctcgg ccgggctgcg caccctctg ctctgcctct tgctcctggc tccccatcac   1320
ctctga                                                             1326
```

<210> 21
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 21
```
Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1               5                  10                  15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
            20                  25                  30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
        35                  40                  45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
    50                  55                  60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65                  70                  75                  80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
                85                  90                  95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
            100                 105                 110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
        115                 120                 125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
    130                 135                 140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145                 150                 155                 160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
                165                 170                 175
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
            180                 185                 190
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
        195                 200                 205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
    210                 215                 220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
225                 230                 235                 240
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
                245                 250                 255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
            260                 265                 270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
        275                 280                 285
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
    290                 295                 300
```

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```
Asp Leu Glu Gly Cys Ala Val Ala Thr Ser Pro Thr Arg Pro Gly Ser
305                 310                 315                 320
Arg Ala Arg Gly Asn Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
                325                 330                 335
Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
                340                 345                 350
Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
            355                 360                 365
Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
        370                 375                 380
Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
385                 390                 395                 400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
                405                 410                 415
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
                420                 425                 430
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
                435                 440                 445
Leu Gly Pro Cys
        450
```

```
<210> 22
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 22
atgaagaggg cgtcctccgg aggaagccgg ctgctggcat gggtgttatg gctacaggcc     60
tggagggtag caacgccctg ccctggtgcc tgtgtgtgct acaatgagcc caaggtcaca    120
acaagctgcc cccagcaggg cctgcaggct gtacccactg gcatcccagc ctccagccag    180
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag ccgccagctt ccagtcatgc    240
cggaatctca ccatcctgtg gctgcactca aatgcgctgg ccgggattga tgccgcggcc    300
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc    360
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc    420
ggcctgcagg agctggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac    480
ctacaagaca acaacctgca ggcacttccc gacaacacct tccgagacct gggcaacctc    540
acgcatctct ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc    600
ttgcacagtc ttgaccgtct cctcttgcac cagaaccatg tggctcgtgt gcacccacat    660
gccttccggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg    720
ctccccgcag aggtcctagt gcccctgagg tctctgcagt acctgcgact caatgacaac    780
ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt    840
tcctcatccg aggtgccctg caacctaccc caacgcctgg caggccgtga tctgaagcgc    900
ctggctgcca gtgacttaga gggttgtgct gtggctacta gacccacgcg gccgggcagc    960
cgcgcccgcg gcaacactag tcccgggagg ccggcgtctg ctggaaatgc actcaaggga   1020
cgtgtgcctc ccggtgacac tccaccaggc aatggctcag gcccacggca catcaatgac   1080
tctccatttg ggactttgcc gggctctgca gagccccccac tgactgccct gcggcctggg   1140
ggttccgagc ccccgggact gcccaccacg ggtccccgca ggaggccagg ttgttccaga   1200
aagaaccgca cccgtagcca ctgccgtctg ggccaggcag gaagtgggag cagtggaact   1260
ggggatgcag aaggttcggg ggccctgcct gccctggcct gcagccttgc tcctctgggc   1320
cttgcactgg tactttggac cgtgctcggg ccctgctga                          1359
```

```
<210> 23
<211> 452
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 23
```
Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
1               5                   10                  15
Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
            20                  25                  30
Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
            35                  40                  45
Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
    50                  55                  60
Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
65                  70                  75                  80
Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
            85                  90                  95
Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
            100                 105                 110
Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
            115                 120                 125
Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
    130                 135                 140
Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
145                 150                 155                 160
Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
                165                 170                 175
Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
            180                 185                 190
Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
            195                 200                 205
Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
    210                 215                 220
Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
225                 230                 235                 240
Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
            245                 250                 255
Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
            260                 265                 270
Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
    275                 280                 285
Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
    290                 295                 300
Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
305                 310                 315                 320
Arg Ala Arg Gly Glu Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
            325                 330                 335
Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
            340                 345                 350
Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
            355                 360                 365
Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
    370                 375                 380
Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
```

```
385                    390                    395                    400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
                    405                    410                    415
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
                    420                    425                    430
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
                    435                    440                    445
Leu Gly Pro Cys
        450
```

```
<210> 24
<211> 1358
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 24
atgctgcccg ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca    60
ctcctggccc tccctcctgt daccccagc tgccctatgc tctgcacctg ctactcctct   120
ccgcccacag tgagctgcca ggccaacaac ttctcctcgg tgccgctgtc cttgccaccc   180
agtacacagc gactcttctt gcagaacaac ctcattcgct cactgcggcc aggaactttt   240
gggcccaacc tgctcaccct gtggctcttc tccaacaacc tctccaccat ctaccctggc   300
accttccgcc atctgcaggc cctagaggaa ctggacctcg gtgacaatcg gcacctgcgc   360
tccctggagc ctgacacctt ccagggcctg gagaggctgc agtcactaca tctgtaccgg   420
tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagcct acagtacctc   480
tacctccagg agaacagcct gctccaccta caggatgact tgttcgccga cctggccaac   540
ctgagccacc tttcctcca cgggaaccgc ctgcggctgc tcacggagca cgtgttccgc   600
ggcttgggca gcctggaccg gctgctgctg cacgggaacc ggctgcaggg cgtacaccgc   660
gcagccttcc acggtctcag ccgcctcacc atcctttacc tgttcaacaa cagcctggcc   720
tcgctgccgg gagaggcgct ggctgacctg ccagcgctcg agttcctgcg gctcaacgcc   780
aaccccctggg cgtgcgactg ccgcgctcgg ccgctctggg cttggttcca gcgcgcgcgg   840
gtgtccagct ccgacgtgac ctgcgccacc ccgcccgagc gccagggccg ggacctgcgc   900
acgctgcgcg acaccgattt ccaagcgtgc ccgccgccca cacccacgcg gccgggcagc   960
cgcgcccgcg ggaaactagt cccgggaggc cggcgtctgc tggaaatgca ctcaagggac  1020
gtgtgcctcc cggtgacact ccaccaggca atggctcagg cccacggcac atcaatgact  1080
ctccatttgg dactttgccg ggctctgcag agcccccact gactgccctg cggcctgggg  1140
gttccgagcc cccgggactg cccaccacgg gtccccgcag gaggccaggt tgttccagaa  1200
agaaccgcac ccgtagccac tgccgtctgg gccaggcagg aagtgggagc agtggaactg  1260
gggatgcaga aggttcgggg gccctgcctg ccctggcctg cagccttgct cctctgggcc  1320
ttgcactggt actttggacc gtgctcgggc cctgctga                         1358
```

```
<210> 25
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 25
Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg
 1                   5                  10                  15
Leu
```

```
<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 26
Thr Ala Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr
 1               5                  10

<210> 27
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 27
His Ser Gly Ala Gly
 1               5

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 28
gccatcccgg agggcatccc                                          20

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
      Synthetic Construct

<400> 29
acacttatag aggtagaggg cgtg                                     24
```